gcggccgccgtacggccATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTT
TCGCTACCGTAGCGCAGGCCGAAGTTAAACTGCATGAGTCAGGGCCTGGGCTGGTAAGGC
CTGGGACTTCAGTGAAGATATCCTGCAAGGCTTCTGGCTACACCTTCACTAACTACTGGC
TAGGTTGGGTAAAGCAGAGGCCTGGACATGGACTTGAGTGGATTGGAGATATTTACCCTG
GAGGTGGTTATACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACA
CATCCTCCAGCACTGCCTACATGCAGCTCAGTAGCCTGACATCTGAGGACTCTGCTGTCT
ATTTCTGTGCAAGATTTTACTACGGTAGTAGCTACTGGTACTTCGATGTCTGGGGCCAAG
GCACCACGGTCACCGTCTCCTCAGCAAAGACCACTCCTCCGTCTGTTTACCCTCTGGCTC
CTGGTTCTGCGGCTCAGACTAACTCTATGGTGACTCTGGGATGCCTGGTCAAGGGCTATT
TCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACACCT
TCCCAGCTGTCCTGCAATCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCA
GCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCTTCTAGCACCAAAG
TTGACAAGAAAATCGTACCGCGCGACTGCTAAccgtag<u>taaqaaaaacttaqqqtqaaaq</u>
ttcatcgc<u>ggcc</u>gtacggccATGAAACAAAGCACTATTGCACTGGCACTCTTACCGTTAC
TGTTTACCCCTGTGACAAAAGCCGACATCGAGCTCACCCAGTCTCCAGCAATCATGGCTG
CATCTGTGGGAGAAACTGTCACCATCACATGTGGAGCAAGTGAGAATATTTACGGTGCTT
TAAATTGGTATCAGCGGAAACAGGGAAAATCTCCTCAGCTCCTGATCTATGGTGCAACCA
ACTTGGCAGATGGCATGTCATCGAGGTTCAGTGGCAGTGGATCTGGTAGACAGTATTCTC
TCAAGATCAGTAGCCTGCATCCTGACGATGTTGCAACGTATTACTGTCAAAATGTGTTAA
GTACTCCTCGGACGTTCGGAGCTGGGACCAAGCTCGAGCTGAAGCGCGCTGATGCTGCAC
CGACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCG
TGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCT
ACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATA
CCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATG
AGTGTTAGtccgtag<u>taaqaaaaacttaqqqtqaaaq</u>ttcatgcggccgc

FIG. 1

SYN80 F1: CGGAATTCGCGGCCGCCGTACGGCCATGAAAAAGACAGCTATCGCGATTGCGAGTGGCACTGGCTGGTT (SEQ ID NO:12)
SYN80 F2: TGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCCGAAGTTAAACTGCATGAGTCAGGGCCTGGG (SEQ ID NO:13)
SYN80 F3: TGCATGAGTCAGGGCCTGGGCTGGTAAGGCCTGGGACTTCAGTGAAGATATCCTGCAAGGCTTCTGGCTA (SEQ ID NO:14)
SYN80 F4: ACTGCAGACACATCCTCCAGCACTGCCTACACTGCAGCTCAGCTCAGTAGCCTGACATCTGAGGAC (SEQ ID NO:15)
SYN80 F5: GTAGCCTGACATCTGCTGCTGTCTATTCTGTGCAAGATTTTACTACGGTAGTA (SEQ ID NO:16)
SYN80 F6: AAGATTTTACTACGGTAGTAGCTACTTGTACTTCGATGTCTGGGGCCAAGGCACCACGGT (SEQ ID NO:17)
SYN80 F7: CGGGATCCCTGTCCAGCGGTGTGCACACTTCCCAGCTGTCCTGCAATCTGACCTCTACA (SEQ ID NO:18)
SYN80 F8: CCTGCAATCTGACCTCTACACTCTGAGCAGCTCTACACTGCCCAGCGAGACC (SEQ ID NO:19)
SYN80 F9: GCACCTGGCCCAGCGAGACCGTCACCTGACCTGCCCACCCGGCTTCTAGCACCAAAGTTGACAAGAA (SEQ ID NO:20)
SYN80 F10: GCCGACATCGAGCTCACCCAGTCTCCAGCAATCATGGCTGTGTGGGAGAAACTGTCACCATCACAT (SEQ ID NO:21)
SYN80 F11: AGAAACTGTCACCATCACATGTCGAGCAAGTGAGAATATTACGGTGCTTTAAATTGGTATCAGCGGAAA (SEQ ID NO:22)
SYN80 F12: TAAATTGGTATCAGCGGAAACAGGAAAATCTCCTCAGCTCCTGATCTATGGTGCAACCAACTTGGCAGA (SEQ ID NO:23)
SYN80 F13: ACCGCTCGAGCTGAAGCGCGCTGATGCTGAAGGCTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAAC (SEQ ID NO:24)
SYN80 F14: CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCTGTGCTTCTTGAACAACTTCTACCCCAAAG (SEQ ID NO:25)
SYN80 F15: GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTC (SEQ ID NO:26)
SYN80 R1: CAAGAGCTTCAACAGGAATGAGTGTTAGTCCTGAGTAAGAAAAACTTAGGTGAAGTTCATGCGGCCGCAAGCTTGGG (SEQ ID NO:27)
SYN80 R2: TGAACGACATAACAGCTATACCTGTGGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATG (SEQ ID NO:28)
SYN80 R3: GACAGCACCTACAGCATGAGGTTCCTGAACAGTTGGACTGATCAGGACGAGTATGAACGACAGCACCTACAGCTATA (SEQ ID NO:29)
SYN80 R4: GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACGTTCGGAGCGTTCGGAGCCAAGCTTGGG (SEQ ID NO:30)
SYN80 R5: TTACTGTCAAAATGTGTTAAGTACTCCTCGGACGTTCGGAGCCCAAGCTTGGG (SEQ ID NO:31)
SYN80 R6: ATCTGGTAGACAGTATTCTCTCAAGATCAGTAGCCTGCATCCTGACGATGTTGCAACGTATTACTGTCAAAATGTGTTAA (SEQ ID NO:32)
SYN80 R7: GGTGCAACCAACTTGGCATGTCAGATGGCATGTCATCGAGGTTCAGTGGCAGTGGATCTGGTAGACAGTATTCTC (SEQ ID NO:33)
SYN80 R8: GCACTATTGCACTGGCACTCTTACCGTTACTGTTTACCCTGTGACAAAAGCCGACATCGAGCTCACCCA (SEQ ID NO:34)
SYN80 R9: AGAAAACTTAGGTGAAGTTCATCGCGGCCGCATGAAACAAAGCACTATTGCACTGCACTC (SEQ ID NO:35)
SYN80 R10: AGCACCAAAGTTGACAAGAAAATCGTACCGCGCGACTGCTAACCGTAGTAAGAAAACTTAGGTGAAAG (SEQ ID NO:36)
SYN80 R11: TGACTCTGGGATGCCTGGTCAAGGGCTATTTCCCGGCTCAGCCAGTGGCCAGTGCTAACTCTGGATCCCG (SEQ ID NO:37)
SYN80 R12: GTCTGTTTACCCTCCTGGTTCTCGCGGTCTCCTGGTTCTCGCGGTCTCCTGGATGCCTGGTC (SEQ ID NO:38)
SYN80 R13: TGGGGCCAAGGCACCACGGTCACCGTCACCGGTCTCCTGGTTCTCCTCAGCAAGAACCACTCCTCCGTCTGTTTACCCTCCTGGCTC (SEQ ID NO:39)
SYN80 R14: GAGGTGGTTATACTACGGAGGAGTGGTTCTTGCTGAGGAGATATTTACCCTGGAGTGGTGGTTATACTAACTAC (SEQ ID NO:40)
SYN80 R15: AAAGCAGAGCCGTTGGCACATGGAGCTTGGTAGCTTGAGTTCAGGCAAGGGCCACCACTGACTGCAGACACATCCTCCAG (SEQ ID NO:41)
SYN80 R16: TCCTGCAAGGCTTCTGGCTACACCTTCACTAACTACTGGATGCACTGGGTAAAGCAGAGGCCTGGACATG (SEQ ID NO:42)
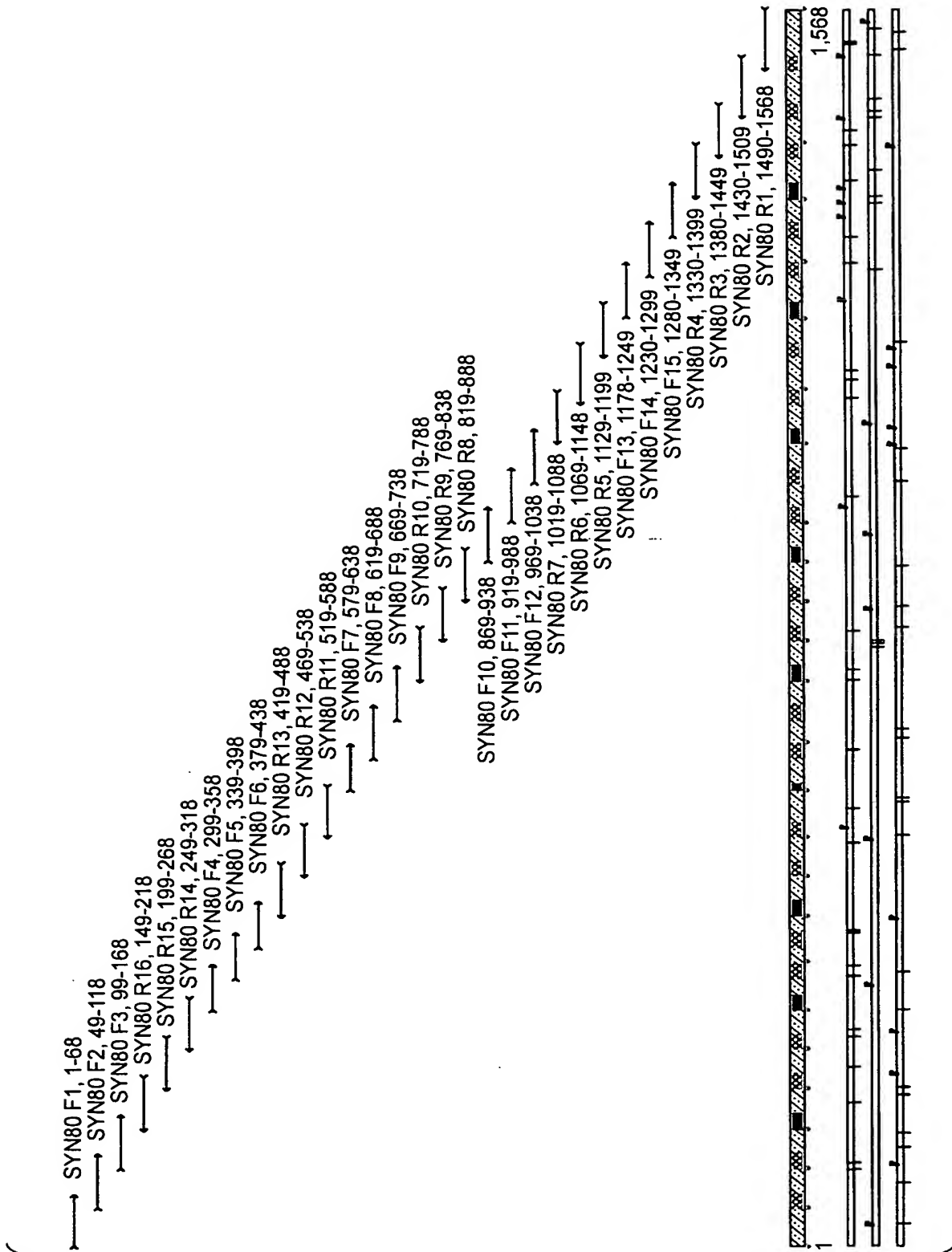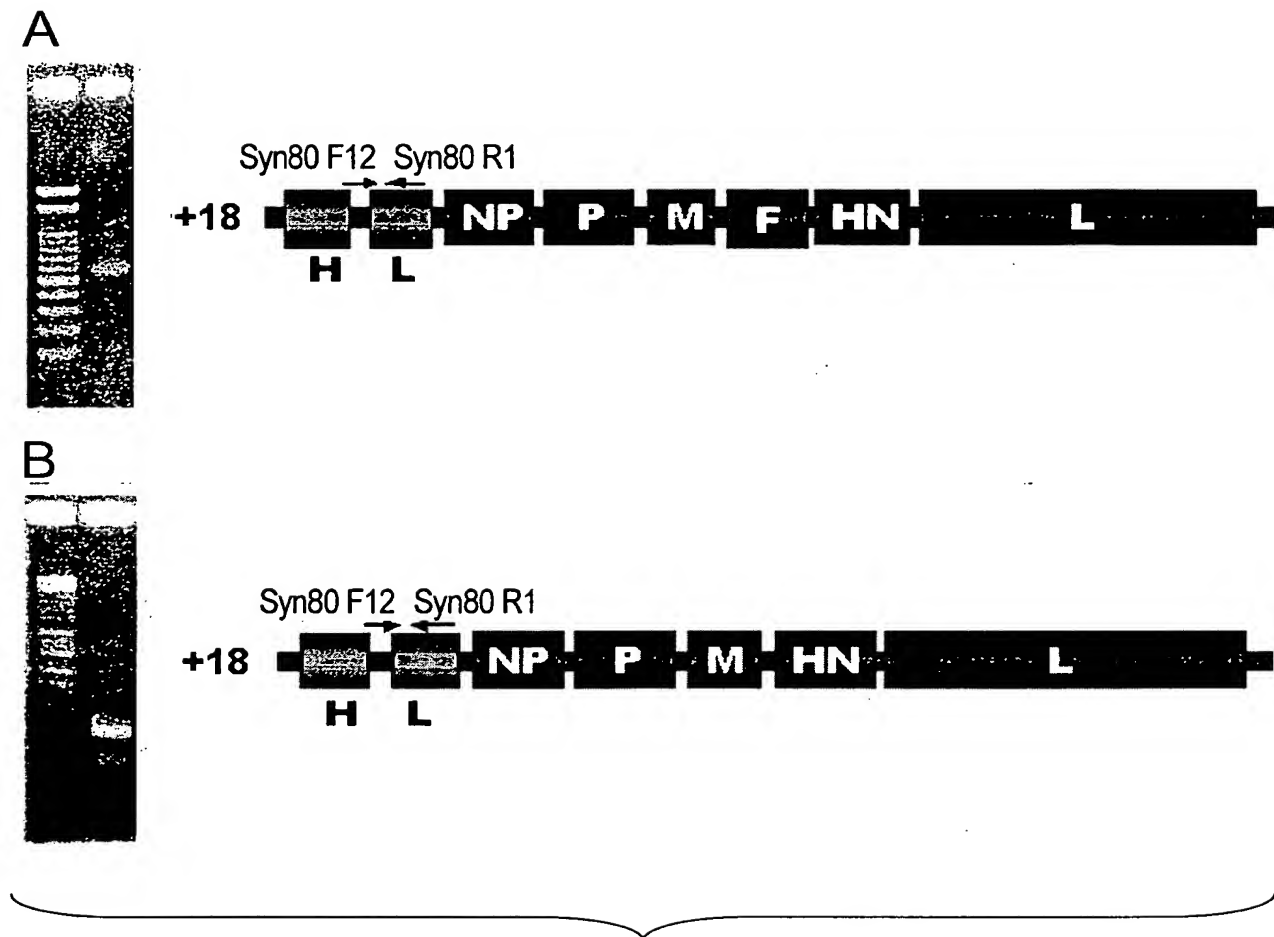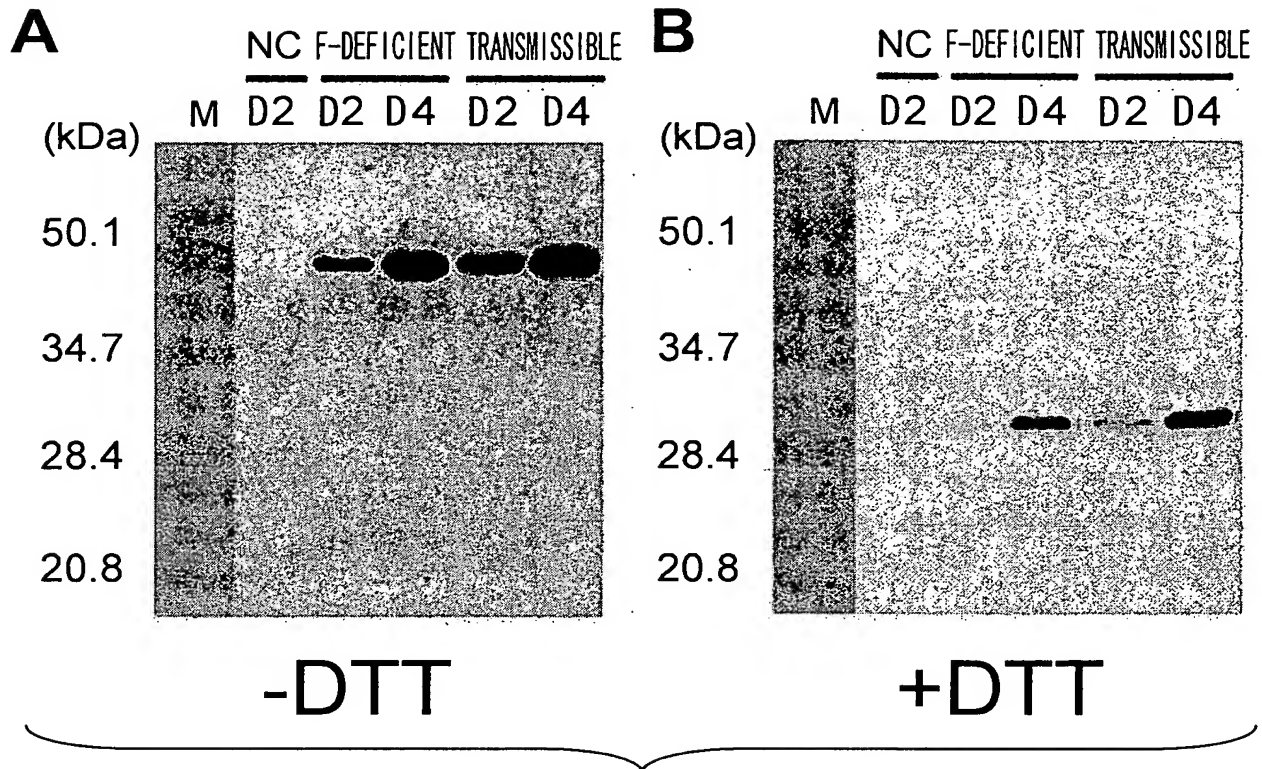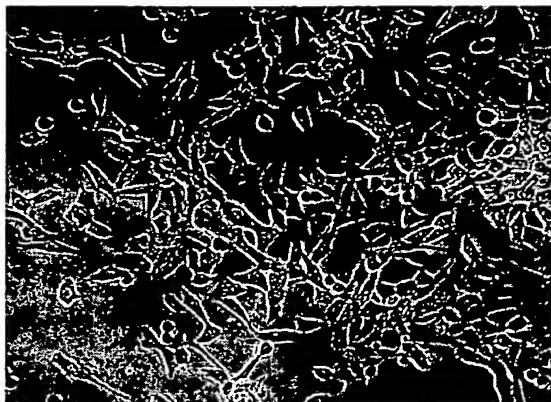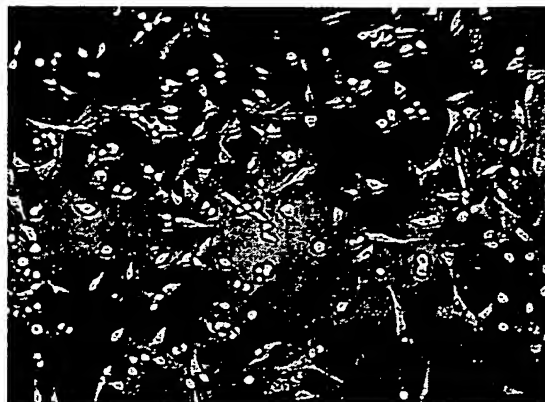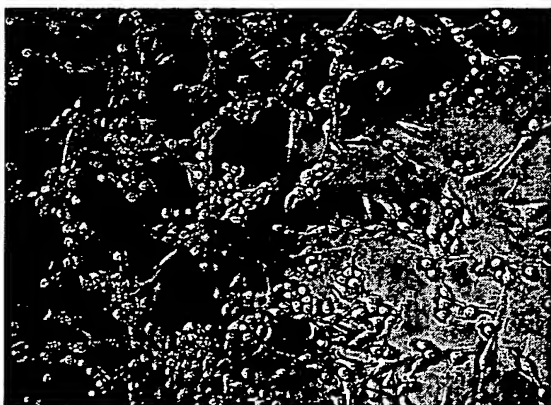
FIG. 2

FIG. 3

FIG. 4

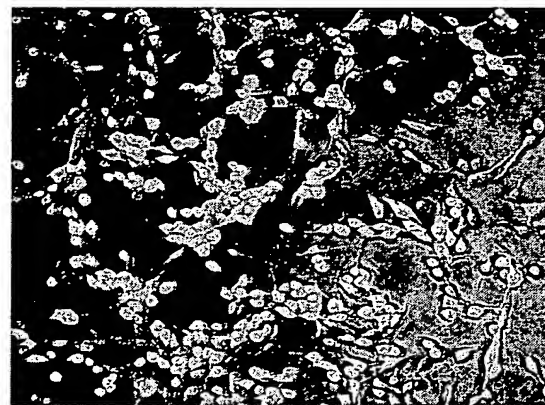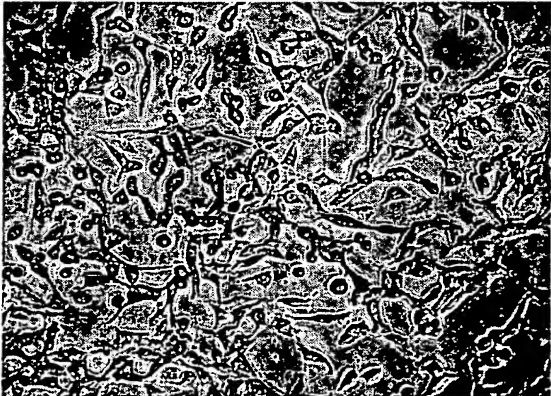FIG. 5

(A) — q-pool

(B) + q-pool

(C) + q-pool: SeV^{18}+GFP
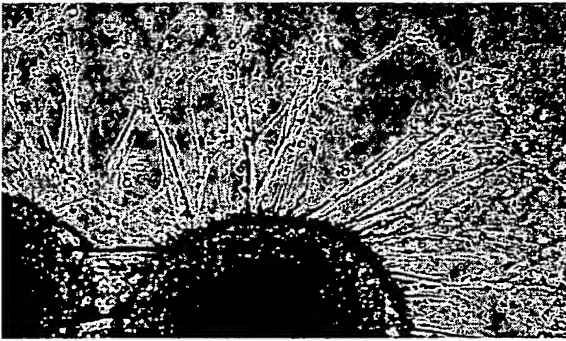
(D)

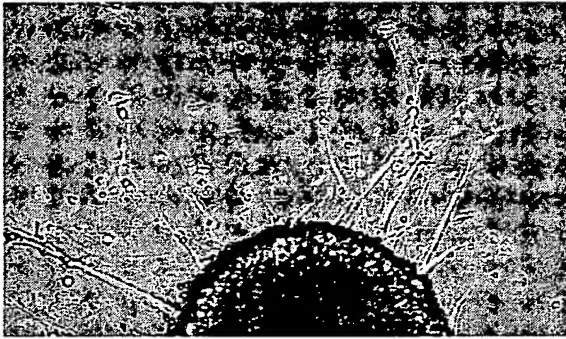(E) + q-pool: SeV^{18}+IN-1

FIG. 6
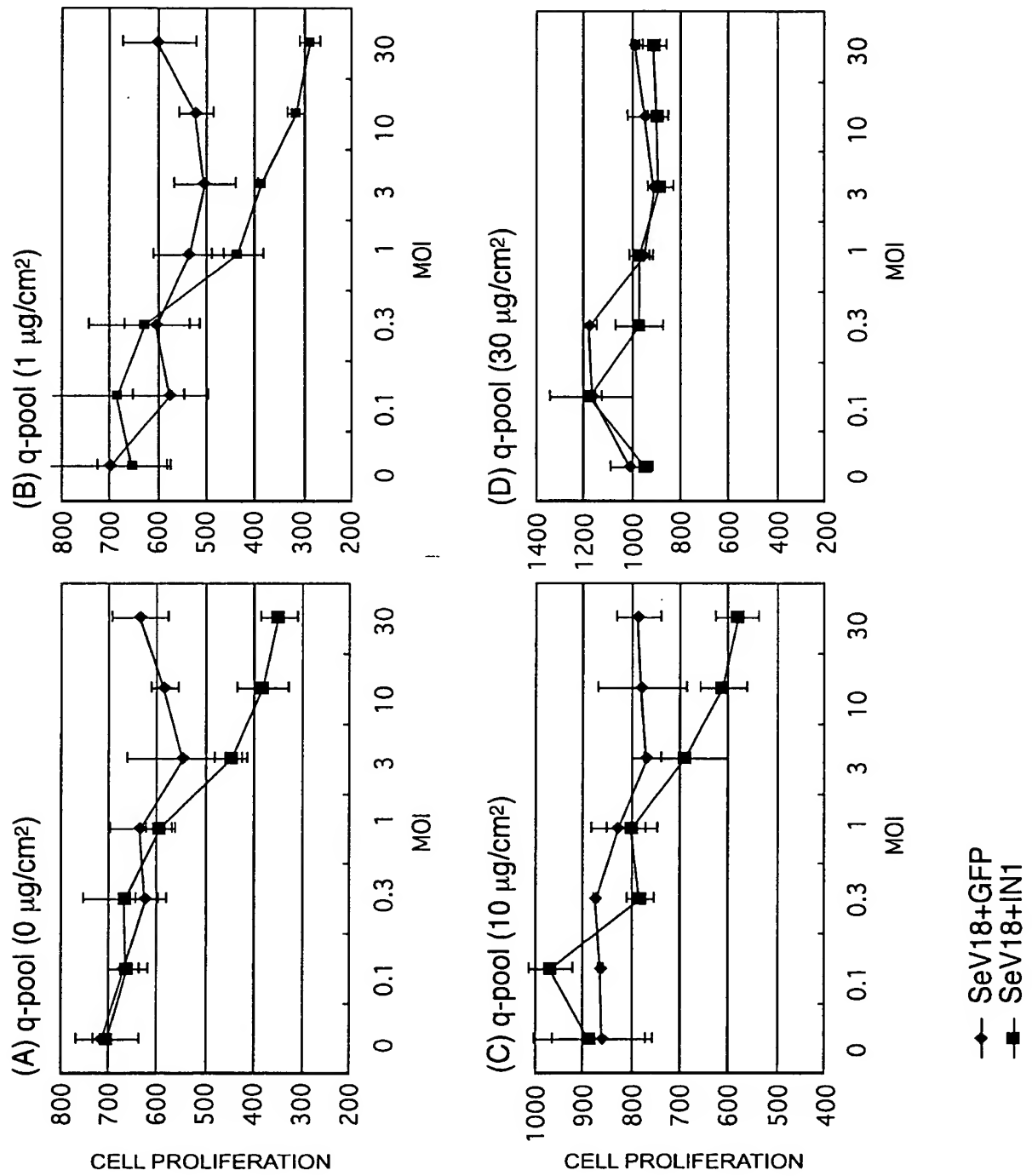
FIG. 7

(A) - q-pool (SeV^{18+}GFP)

(B)
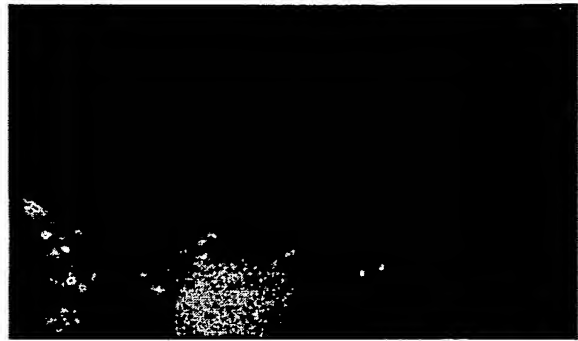
(C) + q-pool (SeV^{18+}GFP)

(D)
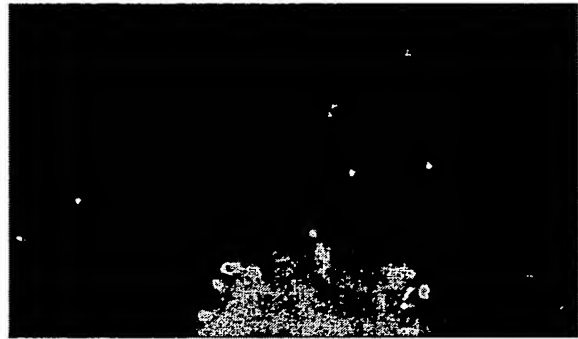
(E) + q-pool (SeV^{18+}IN-1)   -1
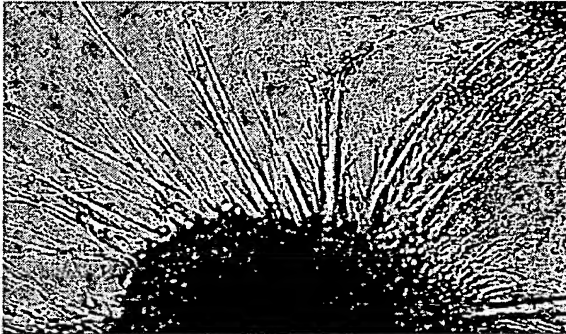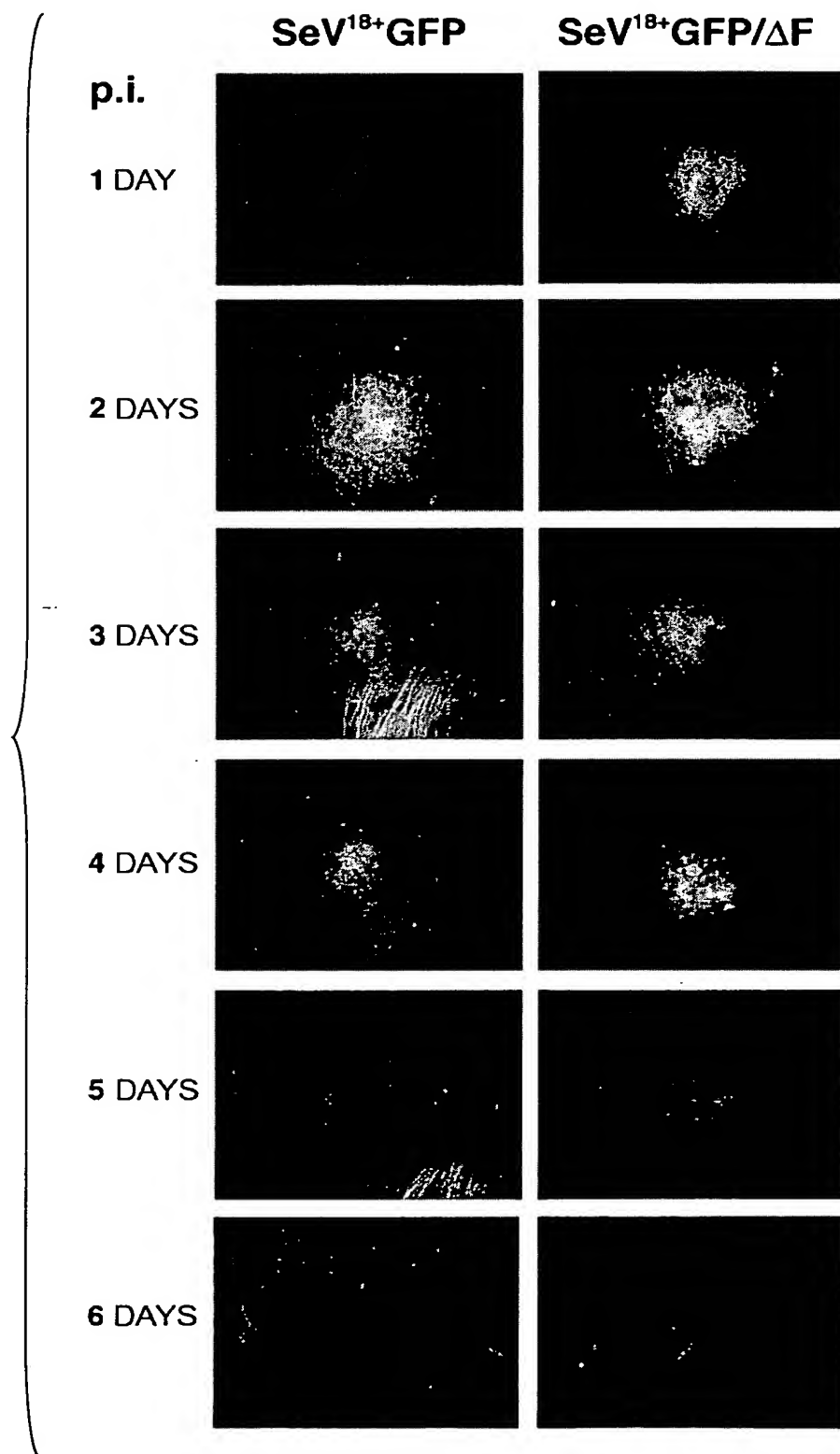
(F) + q-pool (SeV^{18+}IN-1)   -2
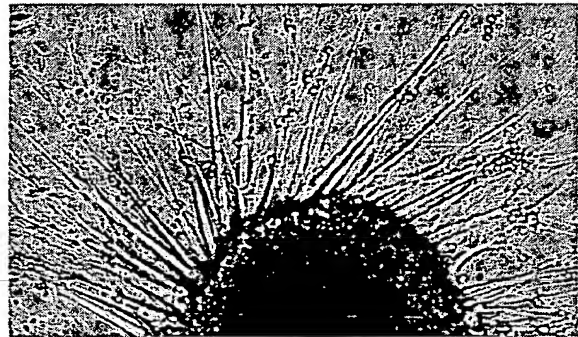
FIG. 8
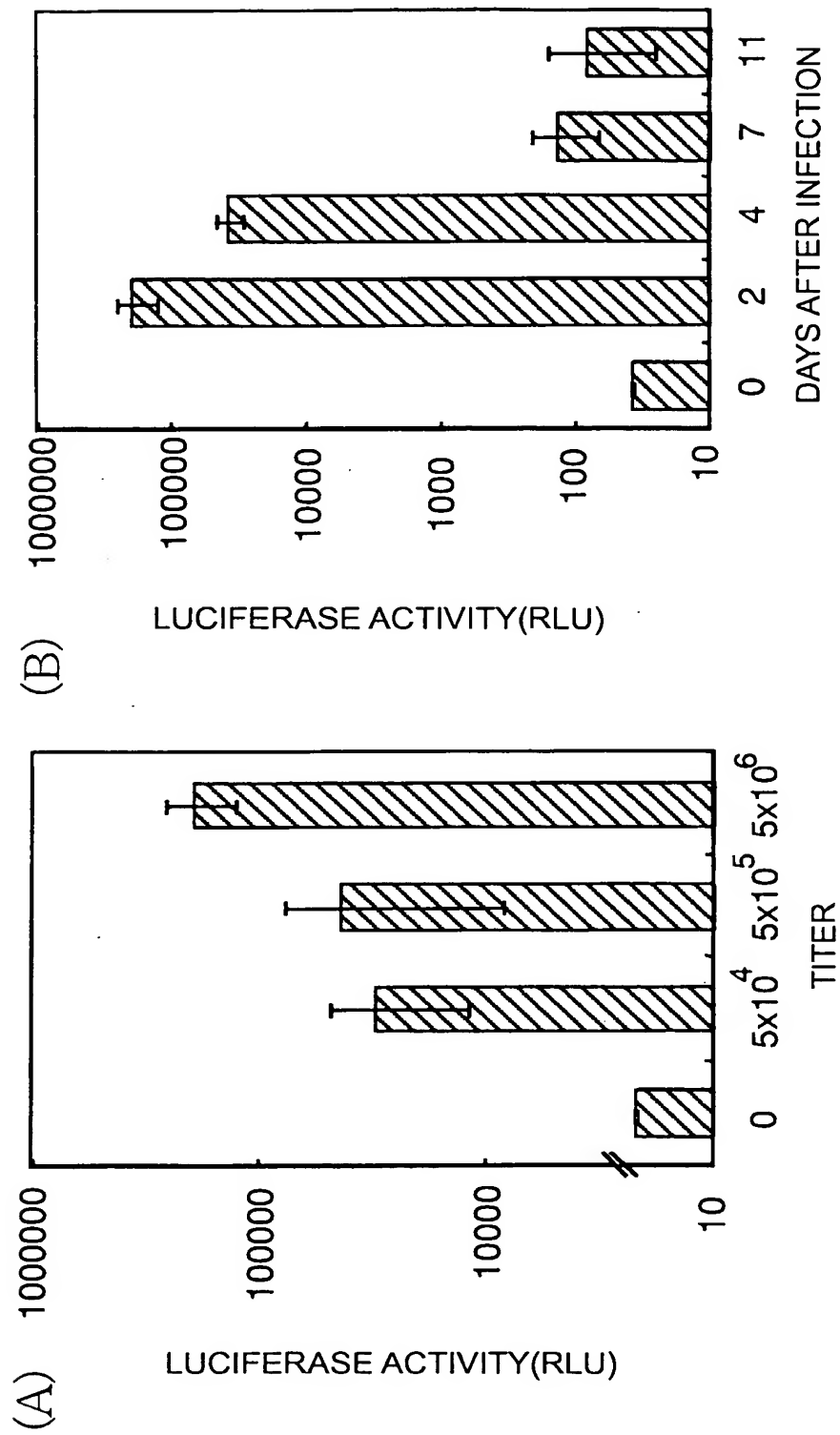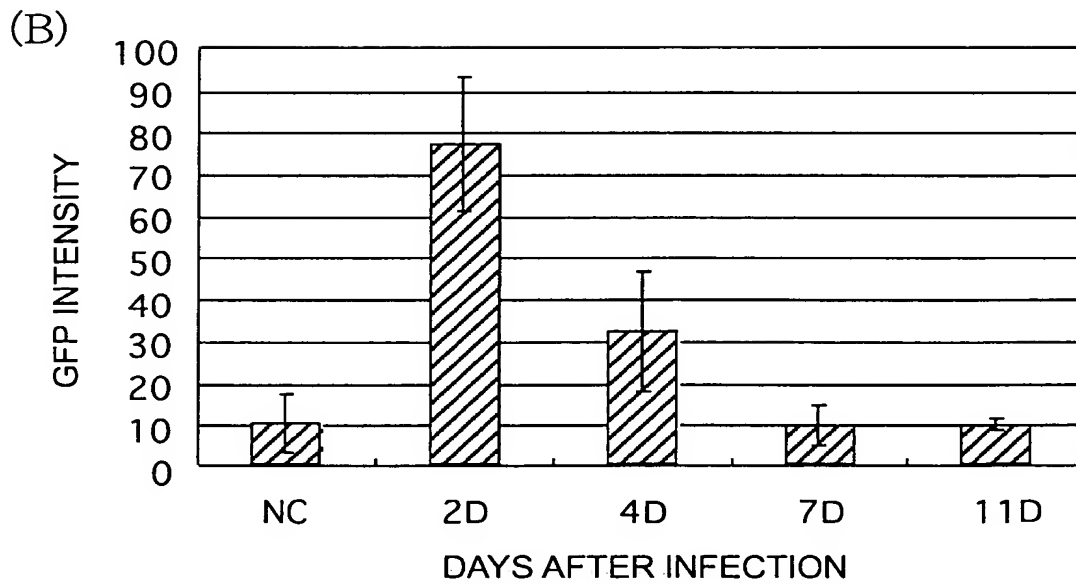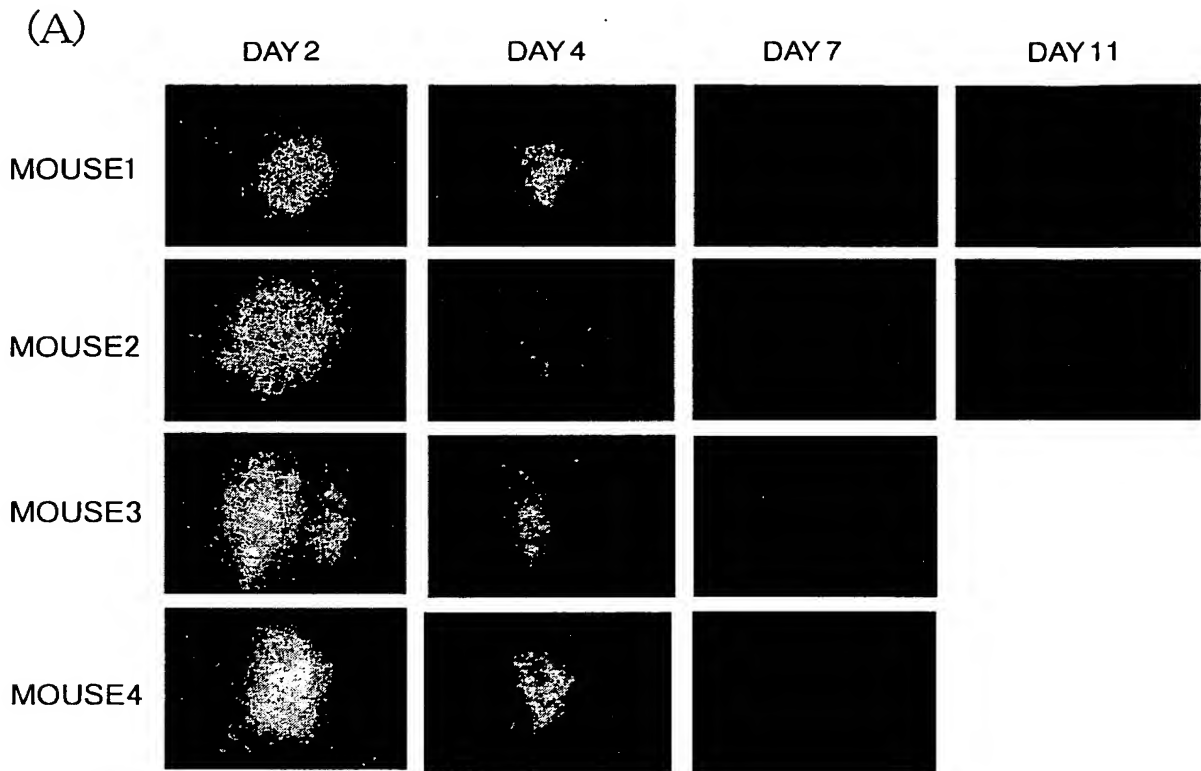
SeV^{18+}GFP   **SeV^{18+}GFP/ΔF**

p.i.

1 DAY

2 DAYS

3 DAYS

4 DAYS

5 DAYS

6 DAYS

FIG. 9

FIG. 10

(A)

	DAY 2	DAY 4	DAY 7	DAY 11
MOUSE1				
MOUSE2				
MOUSE3				
MOUSE4				

(B)

FIG. 11

FIG. 12

FIG. 13

(A)

(B)

(C)

FIG. 14

SYN205 F01, 1 — 70

SYN205 F02, 51 — 120

SYN205 F03, 101 — 170

SYN205 R07, 151 — 220

SYN205 R06, 201 — 270

SYN205 R05, 251 — 320

SYN205 F04, 301 — 370

SYN205 F05, 351 — 420

SYN205 F06, 401 — 470

SYN205 R04, 451 — 520

SYN205 R03, 501 — 570

SYN205 R02, 551 — 620

SYN205 F07, 601 — 670

SYN205 F08, 651 — 720

SYN205 R01, 701 — 753

1   49   100   150   200   250   301   350   401   450   499   550   600   650   753

FIG. 15

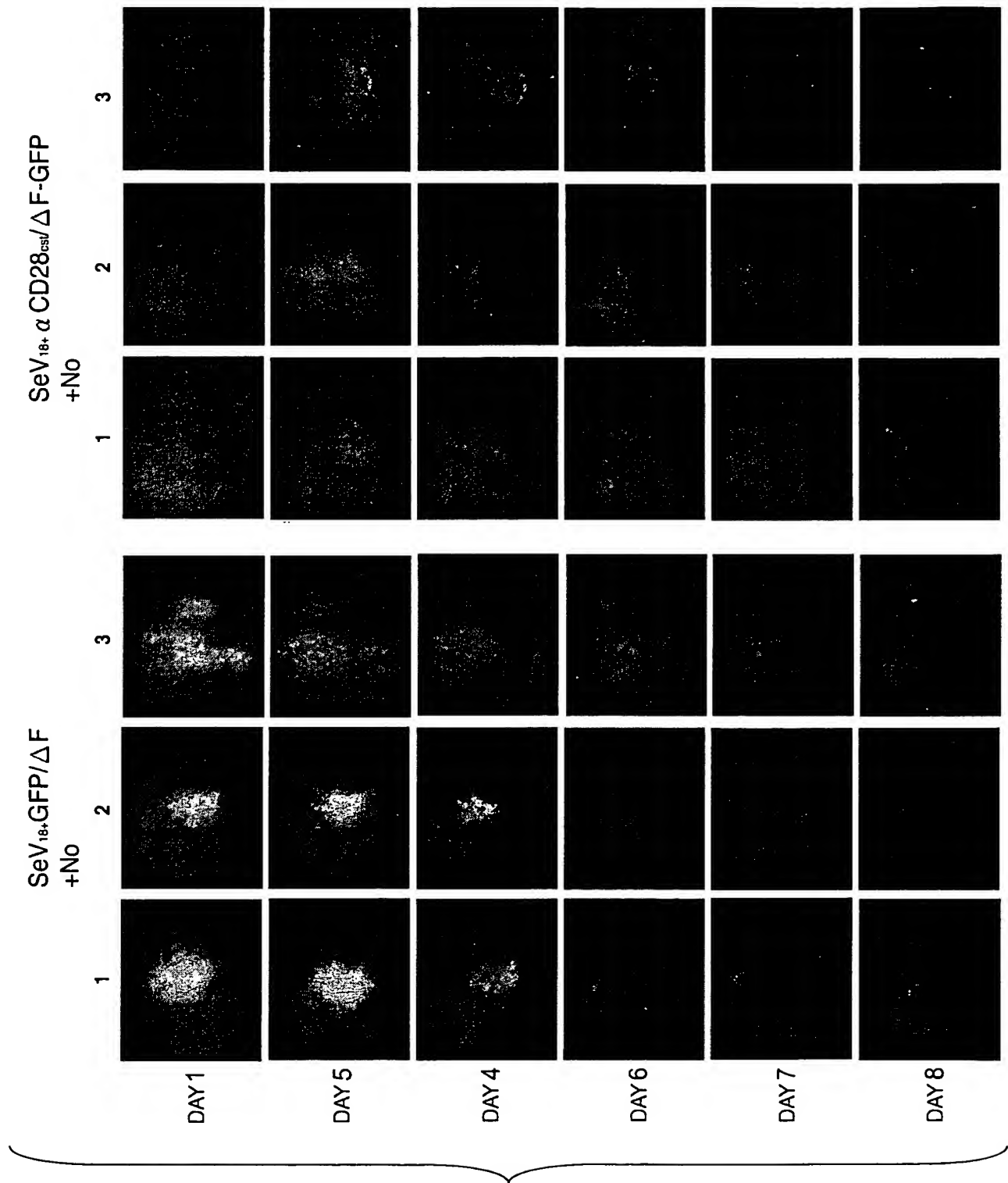FIG. 16

FIG. 17

WESTERN BLOTTING   CBB STAINING
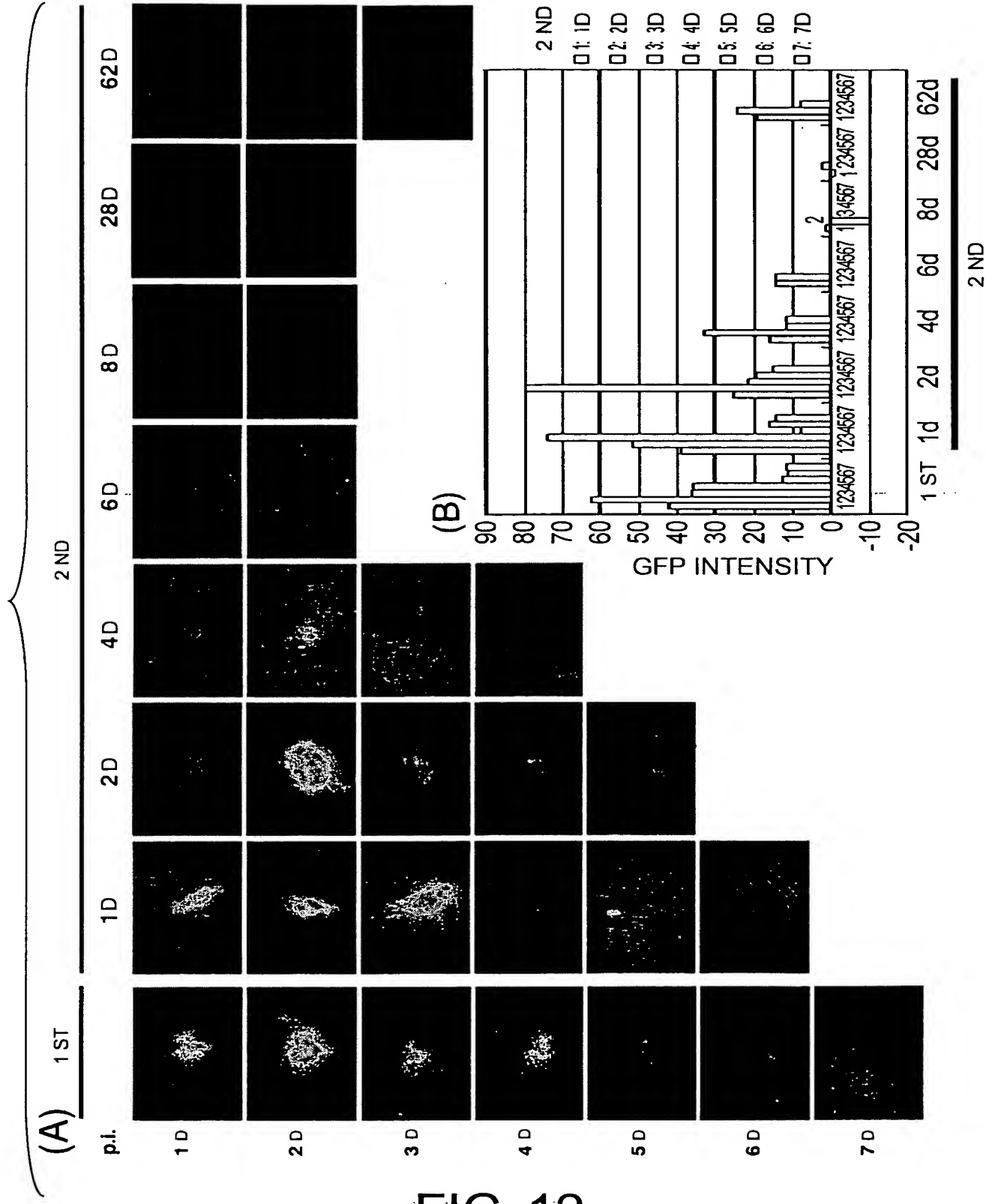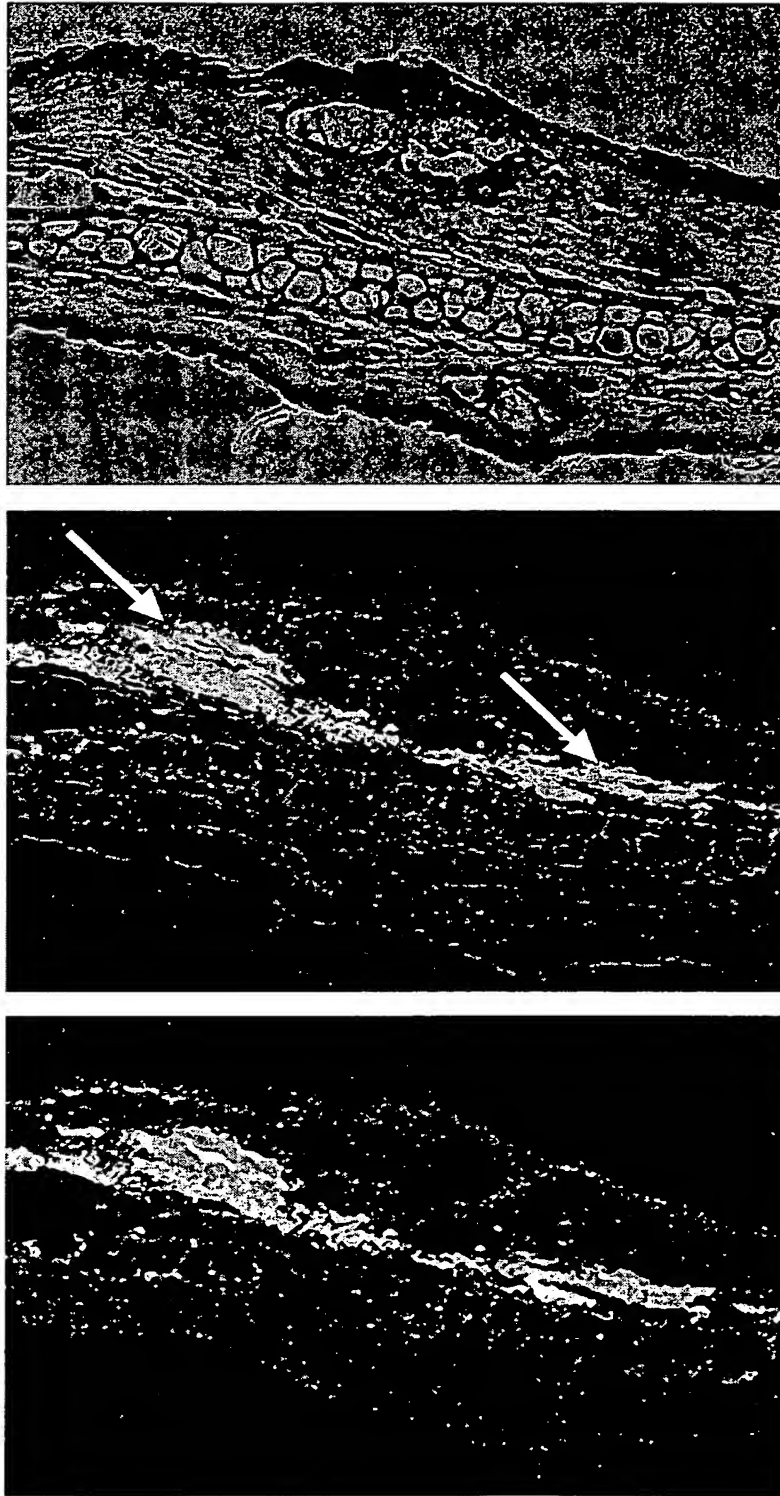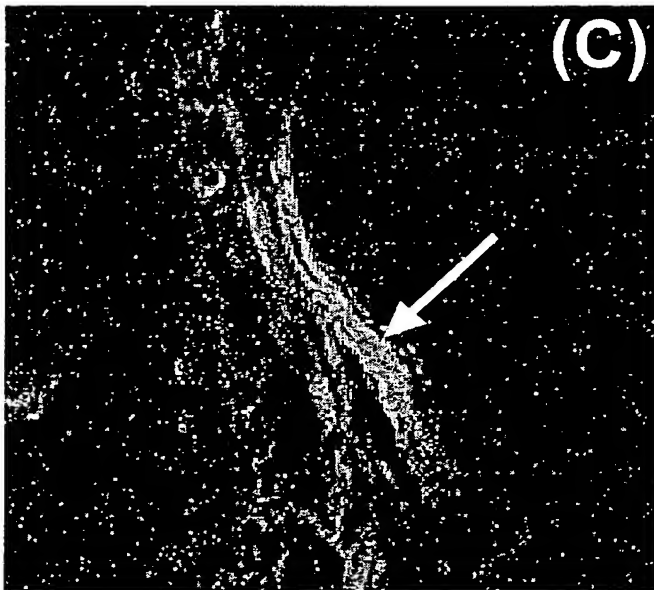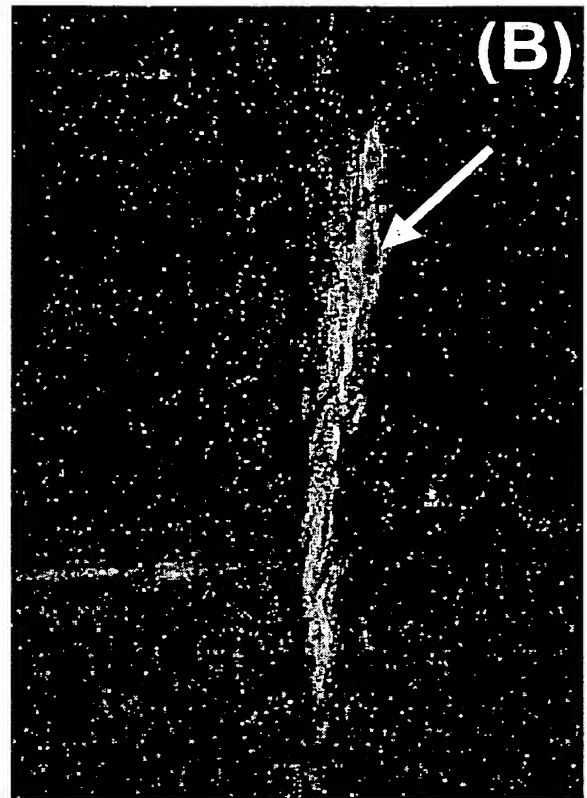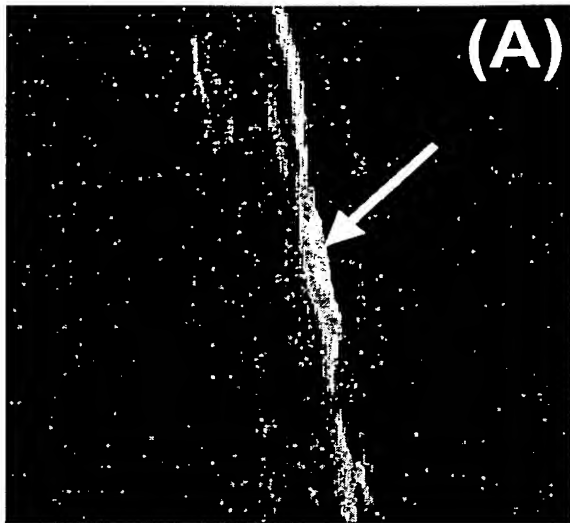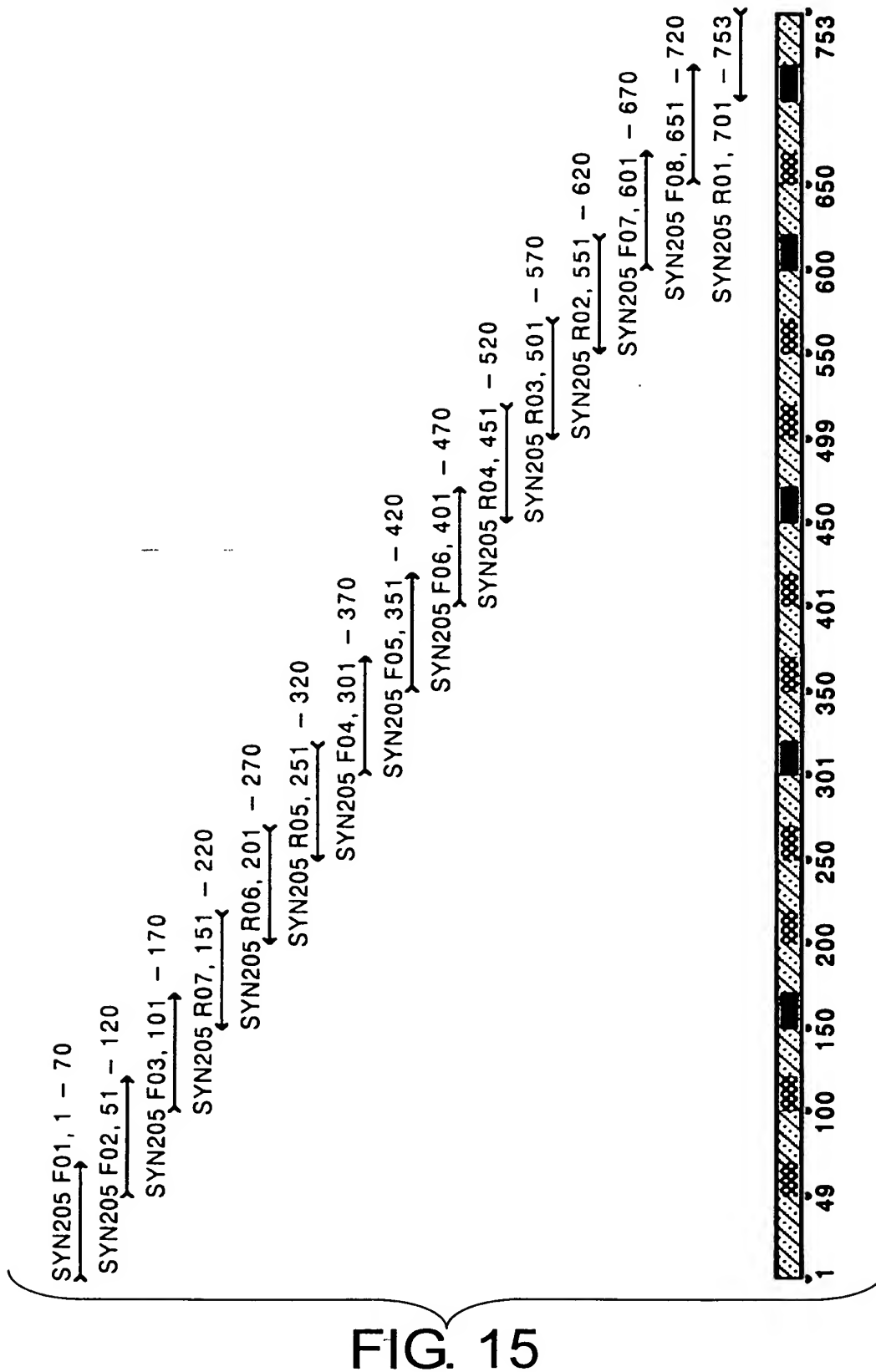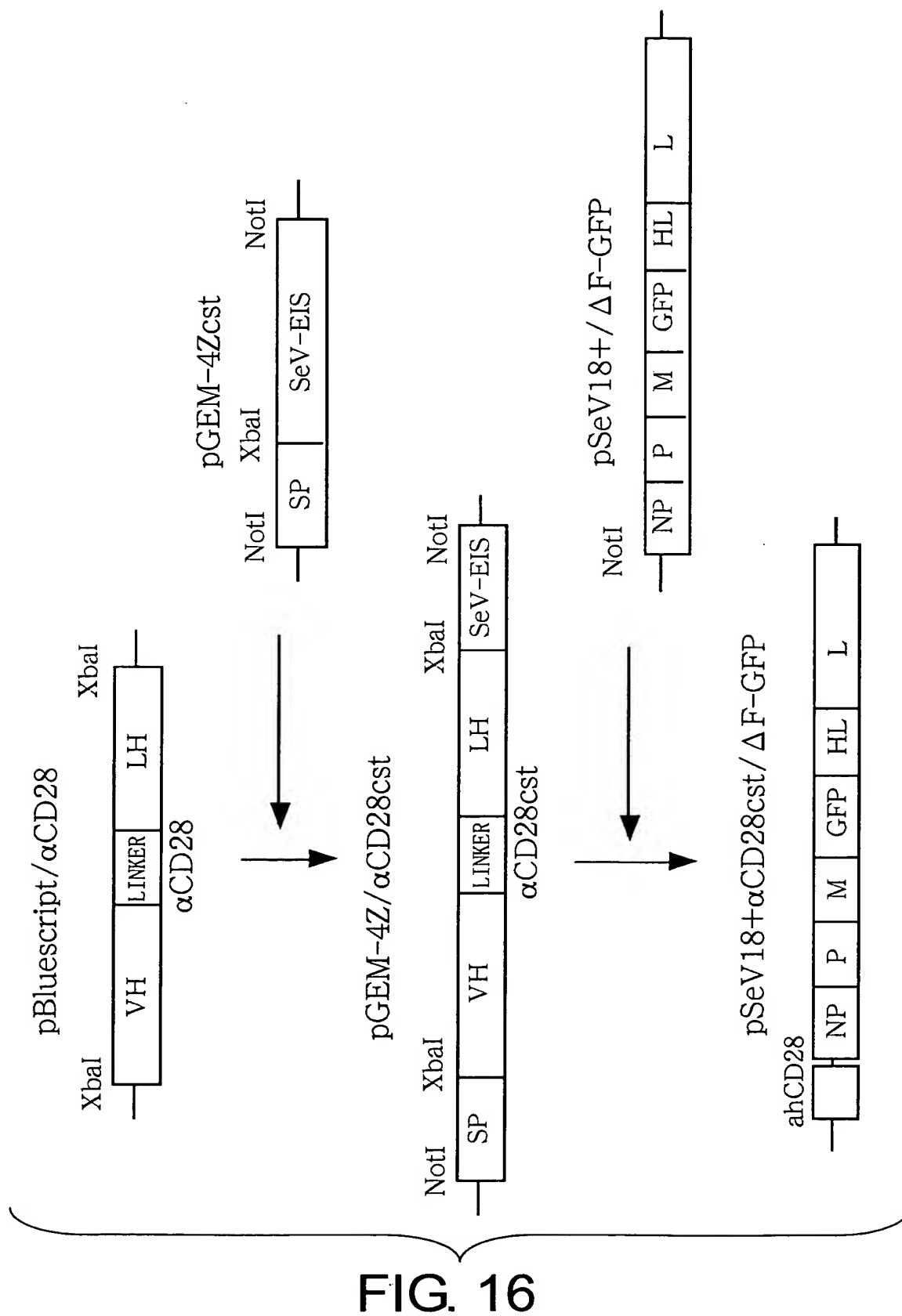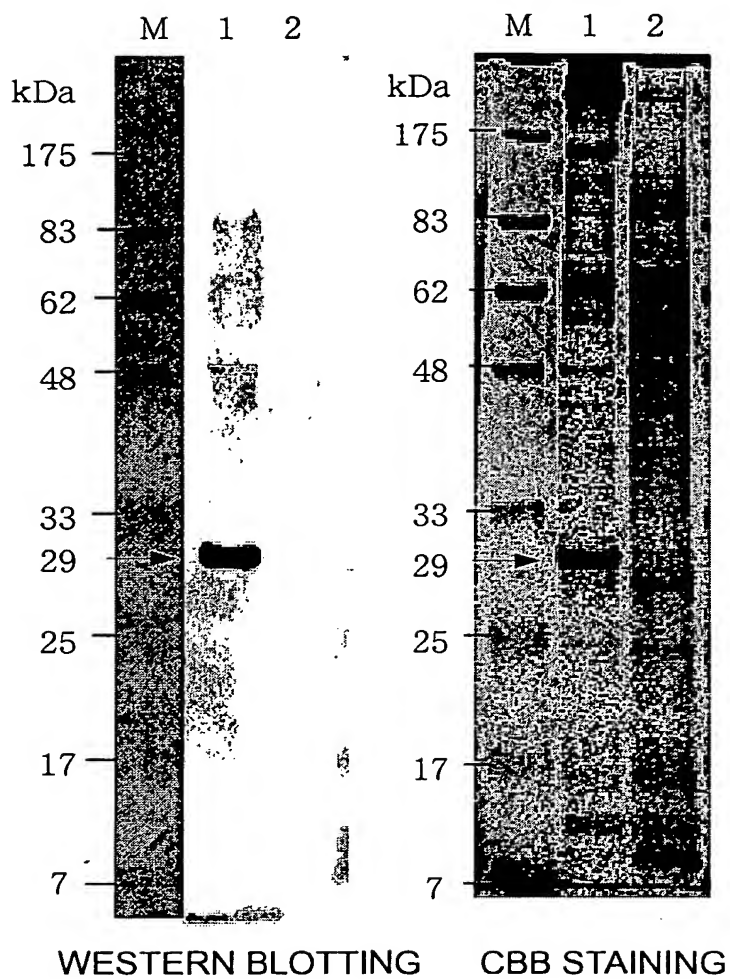
M:PROTEIN MARKER
1: SeV18+αCD28cst/ΔF-GFP CULTURE
                                SUPERNATANT
2: SeV/ΔF(GFP)CULTURE SUPERNATANT

FIG. 18

FIG. 19

SeV₁₈₊GFP/△F
+mCTLA4-Ig PROTEIN(i.p.X2)

SeV₁₈₊ α CD28cst/△F-GFP
+mCTLA4-Ig PROTEIN(i.p.X2)

FIG. 20

FIG. 21

FIG. 22